AMENDMENTS TO THE CLAIMS

1. (currently amended) A method of identifying individuals predisposed to schizophrenia comprising:

a) providing a nucleic acid from a human subject; wherein said nucleic acid comprises an α7 allele;

b) detecting the presence of at least one polymorphism within a core promoter region ~~corresponding to SEQ ID NO:125~~ of said α7 allele, wherein said core promoter region corresponds to SEQ ID NO:125, and wherein said at least one polymorphism contributes to reduced transcription; [[and]]

c) correlating the presence of said at least one polymorphism with a predisposition to schizophrenia; and

d) providing a diagnosis of schizophrenia to said subject based on the presence of said at least one polymorphism and a physician interview.

2. (currently amended) The method of Claim 1, wherein said at least one polymorphism comprises ~~one or more of a -241 A to G substitution, a -194 G to C substitution, a -191 G to A substitution, a -178 G deletion, a -143 G to A substitution, a -92 G to A substitution, and~~ a -86 C to T substitution in relation to a start codon of said α7 allele beginning at residue 270 of SEQ ID NO:125.

3-4. (canceled)

5. (original) The method of Claim 1, wherein said detecting step is accomplished using at least one technique selected from the group consisting of polymerase chain reaction, heteroduplex analysis, single stand conformational polymorphism analysis, denaturing high performance liquid chromatography, ligase chain reaction, comparative genome hybridisation, Southern blotting and sequencing.

6. (original) The method of Claim 1, wherein said nucleic acid from said subject is derived from a sample selected from the group consisting of a biopsy material and blood.

7. (canceled)

8. (currently amended) The method of ~~Claim 7,~~ Claim 1, wherein said diagnosis differentiates schizophrenia from other forms of mental illness.

9-25. (canceled)

26. (currently amended) A method of identifying individuals predisposed to schizophrenia comprising:

a) providing a nucleic acid from a human subject; wherein said nucleic acid comprises an α7 allele;

b) detecting the presence of at least one polymorphism within said α7 allele, wherein said at least one polymorphism comprises ~~one or more of a -241 A to G substitution, a -194 G to C substitution, a -191 G to A substitution, a -180 G to C substitution, a -178 G deletion, a -143 G to A substitution, a -92 G to A substitution, and~~ a -86 C to T substitution in relation to a start codon of said α7 allele beginning at residue 270 of SEQ ID NO:125; and

c) correlating the presence of said at least one polymorphism with a predisposition to schizophrenia.

27-34. (canceled)

35. (previously presented) The method of Claim 26, wherein said detecting step is accomplished using at least one technique selected from the group consisting of polymerase chain reaction, heteroduplex analysis, single stand conformational polymorphism analysis, denaturing high performance liquid chromatography, ligase chain reaction, comparative genome hybridisation, Southern blotting and sequencing.

36. (previously presented) The method of Claim 26, wherein said nucleic acid from said subject is derived from a sample selected from the group consisting of a biopsy material and blood.

37. (previously presented) The method of Claim 26, further comprising step d) providing a diagnosis of schizophrenia to said subject based on the presence of said at least one polymorphism and a physician interview.

38. (currently amended) The method of ~~Claim 36,~~ Claim 37, wherein said diagnosis differentiates schizophrenia from other forms of mental illness.